

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Vinik, Aaron
Pittenger, Gary
Rafaeloff, Ronit
Barlow, Scott

(ii) TITLE OF THE INVENTION: HIGH LEVEL EXPRESSION OF
INGAP

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Witcoff, Ltd.
(B) STREET: 1001 G Street, N.W.
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/741,096
(B) FILING DATE: 30-OCT-1996
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32,145
(C) REFERENCE/DOCKET NUMBER: 0570.01435

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX: 97430 BMB UT

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCAAGACA GGTACCATGA TGCTTCCCAT GACCCCTGT AGGATGTCTT GGATGCTGCT
TTCCTGCCTG ATGTTCCCTT CTTGGGTGGA AGGT

60
94

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGCAGGATCC CGAAGAATCT CAAAAGAAC T

31

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACCGGCTCG AGTGCTCTTC CTGAGTGAAT CC

32

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGGGATCC CGAAGAAC	TGCCTCTTC ACGTATAACC	TGTCCCTCAAG	60
GCTCTGTAGC CTATGGGTCC	TATTGCTATT CACTGATTT	GATACCACAG ACCTGGTCTA	120
ATGCAGAACT ATCCCTGCCAG	ATGCATTTCT CAGGACACCT	GGCATTCTT CTCAGTACTG	180
GTGAAATTAC CTTCTGTGTC	TCCCTTGTA AGAACAGTTT	GACGGCCTAC CAGTACATCT	240
GGATTGGACT CCATGATCCC	TCACATGGTA CACTACCCAA	CGGAAGTGGAA TGGAAGTGGAA	300
GCAGGTTCCA TGCGCTGACC	TTCTATAACT GGGAGAGGAA	CCCTCTTATT GCTGCTGACC	360
GTGGTTATTG TGCAGTTTG	TCTCAGAAAT CAGGTTTCA	GAAGTGGAGA GATTTTAATT	420
GTGAAAATGA GCTTCCCTAT	ATCTGCAAAT TCAAGGTCTA	GGGCAGTTCT AATTTCAACA	480
GCTTGAAAAT ATTATGAAGC	TCACATGGAC AAGGAAGCAA	GTATGAGGAT TCACTCAGGA	540
AGAGCACTCG AGCCGGTC			558

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Met	Leu	Pro	Met	Thr	Leu	Cys	Arg	Met	Ser	Trp	Met	Leu	Leu	Ser
1															15
Cys	Leu	Met	Phe	Leu	Ser	Trp	Val	Glu	Gly						
20															25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Met	Leu	Pro	Met	Thr	Leu	Cys	Arg	Met	Ser	Trp	Met	Leu	Leu	Ser
1															15
Cys	Leu	Met	Phe	Leu	Ser	Trp	Val	Glu	Gly	Glu	Glu	Ser	Gln	Lys	Lys
20															30
Leu	Pro	Ser	Ser	Arg	Ile	Thr	Cys	Pro	Gln	Gly	Ser	Val	Ala	Tyr	Gly
35															45
Ser	Tyr	Cys	Tyr	Ser	Leu	Ile	Leu	Ile	Pro	Gln	Thr	Trp	Ser	Asn	Ala
50															60
Glu	Leu	Ser	Cys	Gln	Met	His	Phe	Ser	Gly	His	Leu	Ala	Phe	Leu	Leu

19

65	70	75	80
Ser	Thr	Gly	Glu
Ile	Thr	Phe	Val
Ser	Ser	Leu	Val
Leu	Lys	Asn	Ser
			Leu
85		90	95
Thr	Ala	Tyr	Gln
Ile	Tyr	Ile	Trp
Trp	Ile	Gly	Leu
		His	Asp
		Pro	Ser
			His
100		105	110
Thr	Leu	Pro	Asn
Gly	Ser	Gly	Trp
Trp	Lys	Trp	Ser
		Ser	Ser
		Asn	Val
115		120	125
Thr	Phe	Tyr	Asn
Trp	Glu	Arg	Asn
		Pro	Ser
		Ile	Ala
		Ala	Asp
130		135	140
Tyr	Cys	Ala	Val
Leu	Ser	Gln	Lys
		Lys	Ser
		Gly	Phe
			Gln
			Lys
			Trp
145		150	155
Phe	Asn	Cys	Glu
			Asn
			Glu
			Leu
			Pro
			Tyr
			Ile
			Cys
			Lys
			Phe
			Lys
			Val
165		170	175